

**Blast 2 Sequences results**

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Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

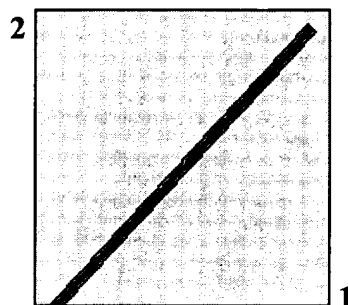
Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ View option **Standard**
Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: lcl|seq_1

Length = 14 (1 .. 14)

Sequence 2: lcl|seq_2

Length = 14 (1 .. 14)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 34.3 bits (77), Expect = 0.76
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 0/14 (0%)

Query 1 AGCKNFFWKTFTSC 14
AGCKNF+WK FTSC
Sbjct 1 AGCKNFYWKGFTSC 14

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H
0.334 0.138 0.589

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 16
Number of extensions: 5
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 14
Length of database: 1,129,354,045
Length adjustment: 0
Effective length of query: 14
Effective length of database: 1,129,354,045
Effective search space: 15810956630
Effective search space used: 15810956630
Neighboring words threshold: 9
X1: 15 (7.2 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 39 (21.7 bits)
S2: 68 (30.8 bits)